

**AMENDMENTS TO THE CLAIMS:**

Claims 21-40 are canceled without prejudice or disclaimer. Claims 1-20 were previously cancelled. The following is the status of the claims of the above-captioned application, as amended.

**Claims 1-20 (Canceled)**

**Claim 41 (New)** A variant of an alpha-amylase having at least 90% homology to SEQ ID NO.8, comprising an alteration at a position corresponding to position 170 in SEQ ID NO:8, wherein the variant has alpha-amylase activity.

**Claim 42 (New)** The variant of claim 41, which variant comprises an alteration at one or more positions selected from the group of: 49, 60, 104, 132, 161, 176, 179, 180, 181, 183, 200, 203, 204, 207, 212, 237, 239, 250, 280, 298, 318, 374, 385, 393, 402, 406, 427, 430, 440, 444, 447, 482 (using SEQ ID NO:8 for numbering).

**Claim 43 (New)** The variant of claim 41, which variant comprises an alteration of K170Q.

**Claim 44. (New)** The variant of claim 41, which variant comprises an alteration of one or more of the following mutations: T49I; D60N; N104D; E132A,V,P; D161N; K170Q; K176R; G179N; K180T; A181N; D183N; D200N; X203Y; D204S; D207V,E,L,G; X212I; K237P; S239W; E250G,F; N280S; X298Q; L318M; Q374R; E385V; Q393R; Y402F; H406L,W; L427I D430N; V440A; N444R,K; E447Q,K; Q482K using SEQ ID NO: 8 for the numbering.

**Claim 45 (New)** The variant of claim 41, wherein the variant has the following mutations:  
K170Q+D207V+N280S;  
E132A+D207V;  
D207E+E250G+H406L+L427I;  
D207V+L318M;  
D60N+D207V+L318M;  
T49I+E132V+V440A;  
T49I+K176R+D207V+Y402F;  
Q374R+E385V+Q393R;

N190F+A209V+Q264S;  
G48A+T49I+G107A+I201F;  
T49I+G107A+I201F;  
G48A+T49I+I201F;  
G48A+T49I+G107A;  
T49I+I201F; T49I+G107A; G48A+T49I;  
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444K+E447Q+Q482K;  
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444K+E447Q+Q482K;  
D161N+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444K+E447Q+Q482K;  
D161N+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+E447Q+Q482K;  
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+E447Q+Q482K;  
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+E447Q+Q482K;  
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N;  
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N;  
H406W+D430N; N444K+E447Q+Q482K; E447Q+Q482K;  
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444R+N444K+E447K+Q482K;  
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444R+N444K+E447K+Q482K;  
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W;  
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W;  
H406W+D430N; N444K+E447K+Q482K; E447K+Q482K;  
N104D+D161N+A181N+D183N+D200N+D204S+K237P+S239W;  
N104D+D161N+A181N+D183N+D200N+D204S+K237P;  
N104D+D161N+A181N+D183N+D200N+D204S;

D161N+A181N+D183N+D200N+D204S+K237P+S239W;

D161N+A181N+D183N+D200N+D204S+K237P;

D161N+A181N+D183N+D200N+D204S; K237P+S239W, using SEQ ID NO: 8 for the numbering.

Claim 46 (New) The variant of claim 41, wherein the variant is derived from a strain of *B. licheniformis*.

Claim 47 (New) The variant of claim 41, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 95%.

Claim 48 (New) The variant of claim 41, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 97%.

Claim 49 (New) The variant of claim 41, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 99%.

Claim 50 (New) The variant of claim 41, wherein the variant consists of an alteration at a position corresponding to position 170 in SEQ ID NO:8.